

Full wwPDB X-ray Structure Validation Report (i)

Oct 16, 2021 – 11:52 PM EDT

PDB ID : 1RK1

Title : Mhc Class I Natural H-2Kb Heavy Chain Complexed With beta-2 Microglob-

ulin and Herpes Simplex Virus Mutant Glycoprotein B Peptide

Authors : Miley, M.J.; Messaoudi, I.; Nikolich-Zugich, J.; Fremont, D.H.

Deposited on : 2003-11-20

Resolution : 2.10 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*A user guide is available at

https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (i)) were used in the production of this report:

MolProbity: 4.02b-467

Mogul : 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : NOT EXECUTED EDS : NOT EXECUTED

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

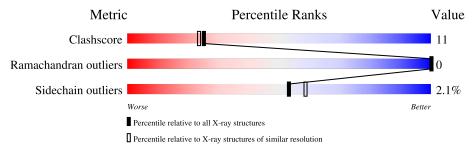
Validation Pipeline (wwPDB-VP) : 2.23.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY\ DIFFRACTION$

The reported resolution of this entry is 2.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{ resolution range}(\AA))$
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain						
1	A	274	82%	17% •					
2	В	99	78%	22%					
3	Р	8	50%	50%					
4	С	2	100%						



2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 3414 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

• Molecule 1 is a protein called H-2 class I histocompatibility antigen, K-B alpha chain.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	A	274	Total 2232	C 1408	N 393	O 422	S 9	0	0	0

• Molecule 2 is a protein called Beta-2-microglobulin.

\mathbf{Mol}	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
2	В	99	Total 821	C 524	N 138	O 152	S 7	0	0	0

• Molecule 3 is a protein called Glycoprotein B.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	Р	8	Total 68	C 43	N 11	O 14	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	2	GLU	SER	engineered mutation	UNP P06436

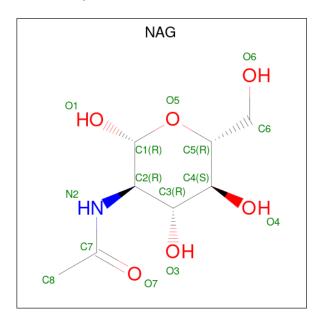
• Molecule 4 is an oligosaccharide called beta-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta -D-glucopyranose.



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace		
4	С	2	Total 24	C 14	N 1	O 9	0	0	0



 \bullet Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6).$



N	Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
	5	A	1	Total 14	C 8	N 1	O 5	0	0

• Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	189	Total O 189 189	0	0
6	В	61	Total O 61 61	0	0
6	Р	5	Total O 5 5	0	0

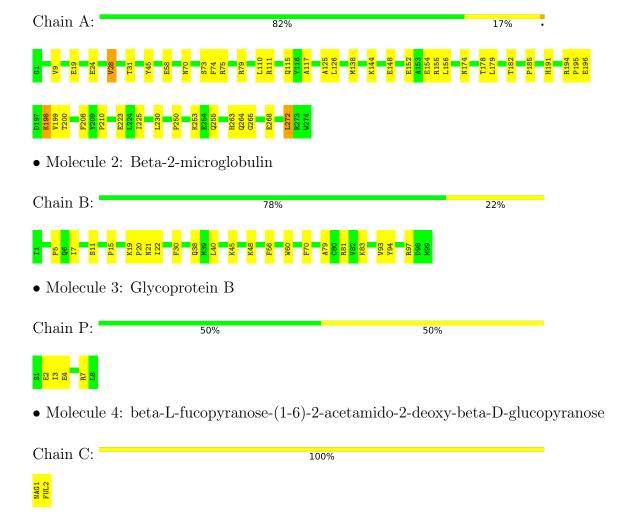


3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

• Molecule 1: H-2 class I histocompatibility antigen, K-B alpha chain





4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source	
Space group	P 21 21 2	Depositor	
Cell constants	135.24Å 89.54Å 45.25Å	Depositor	
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor	
Resolution (Å)	19.97 - 2.10	Depositor	
% Data completeness	95.5 (19.97-2.10)	Depositor	
(in resolution range)	30.9 (13.31 2.10)	-	
R_{merge}	(Not available)	Depositor	
R_{sym}	0.09	Depositor	
Refinement program	CNS 1.1	Depositor	
R, R_{free}	0.208 , 0.230	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	3414	wwPDB-VP	
Average B, all atoms (Å ²)	32.0	wwPDB-VP	



5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, FUL

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with |Z| > 5 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond	lengths	Bond angles		
IVIOI		RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.32	0/2293	0.60	1/3113 (0.0%)	
2	В	0.32	0/847	0.62	0/1148	
3	Р	0.46	0/68	0.64	0/88	
All	All	0.32	0/3208	0.61	1/4349 (0.0%)	

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	28	VAL	N-CA-C	-5.37	96.51	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2232	0	2121	38	0
2	В	821	0	796	23	0
3	Р	68	0	68	5	0
4	С	24	0	22	3	0
5	A	14	0	13	1	0
6	A	189	0	0	6	0
6	В	61	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	Р	5	0	0	0	0
All	All	3414	0	3020	66	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

All (66) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1 Atom-2 Interaction distance (Å) 1:A:75:ARG:HG2 1:A:79:ARG:HH12 1.41 1:A:223:GLU:HB3 1:A:225:ILE:HD13 1.57 2:B:81:ARG:HH12 2:B:83:LYS:NZ 1.79 2:B:19:LYS:HD2 2:B:20:PRO:HD2 1.65 2:B:38:GLN:HE21 2:B:40:LEU:HD21 1.49 1:A:263:HIS:CD2 1:A:265:GLY:H 2.03 1:A:264:GLN:HG3 6:A:927:HOH:O 1.89 5:A:801:NAG:O6 5:A:801:NAG:H2 1.89 2:B:81:ARG:HH12 2:B:83:LYS:HZ2 1.36 2:B:81:ARG:HH22 2:B:83:LYS:HZ1 1.42 2:B:40:LEU:HD23 2:B:45:LYS:HZ 1.76 2:B:38:GLN:NE2 2:B:40:LEU:HD21 2.09 1:A:31:THR:HG21 6:A:1044:HOH:O 1.95 1:A:263:HIS:HD2 1:A:265:GLY:H 1.42 1:A:198:LYS:HB2 1:A:198:LYS:NZ 2.12 1:A:138:MET:HE3 6:A:1028:HOH:O 2.00 2:B:19:LYS:HB2 1:A:198:LYS:HZ3 1.65 1:A:194:ARG:HD2 1:A:200:THR:OG1 2.00 1:A:195:P	0.84 0.84 0.81 0.77 0.77 0.76 0.73 0.72 0.70 0.67 0.67
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1:A:263:HIS:HD2 1:A:265:GLY:H 1.42 1:A:198:LYS:HB2 1:A:198:LYS:NZ 2.12 1:A:138:MET:HE3 6:A:1028:HOH:O 2.00 2:B:19:LYS:HE3 6:B:139:HOH:O 1.99 1:A:198:LYS:HB2 1:A:198:LYS:HZ3 1.65 1:A:194:ARG:HD2 1:A:200:THR:OG1 2.00 1:A:195:PRO:O 1:A:196:GLU:HB2 2.02 1:A:117:ALA:HB2 2:B:60:TRP:CE2 2.38	0.64
1:A:198:LYS:HB2 1:A:198:LYS:NZ 2.12 1:A:138:MET:HE3 6:A:1028:HOH:O 2.00 2:B:19:LYS:HE3 6:B:139:HOH:O 1.99 1:A:198:LYS:HB2 1:A:198:LYS:HZ3 1.65 1:A:194:ARG:HD2 1:A:200:THR:OG1 2.00 1:A:195:PRO:O 1:A:196:GLU:HB2 2.02 1:A:117:ALA:HB2 2:B:60:TRP:CE2 2.38	0.04
1:A:138:MET:HE3 6:A:1028:HOH:O 2.00 2:B:19:LYS:HE3 6:B:139:HOH:O 1.99 1:A:198:LYS:HB2 1:A:198:LYS:HZ3 1.65 1:A:194:ARG:HD2 1:A:200:THR:OG1 2.00 1:A:195:PRO:O 1:A:196:GLU:HB2 2.02 1:A:117:ALA:HB2 2:B:60:TRP:CE2 2.38	0.64
2:B:19:LYS:HE3 6:B:139:HOH:O 1.99 1:A:198:LYS:HB2 1:A:198:LYS:HZ3 1.65 1:A:194:ARG:HD2 1:A:200:THR:OG1 2.00 1:A:195:PRO:O 1:A:196:GLU:HB2 2.02 1:A:117:ALA:HB2 2:B:60:TRP:CE2 2.38	0.63
1:A:198:LYS:HB2 1:A:198:LYS:HZ3 1.65 1:A:194:ARG:HD2 1:A:200:THR:OG1 2.00 1:A:195:PRO:O 1:A:196:GLU:HB2 2.02 1:A:117:ALA:HB2 2:B:60:TRP:CE2 2.38	0.62
1:A:194:ARG:HD2 1:A:200:THR:OG1 2.00 1:A:195:PRO:O 1:A:196:GLU:HB2 2.02 1:A:117:ALA:HB2 2:B:60:TRP:CE2 2.38	0.62
1:A:195:PRO:O 1:A:196:GLU:HB2 2.02 1:A:117:ALA:HB2 2:B:60:TRP:CE2 2.38	0.61
1:A:117:ALA:HB2 2:B:60:TRP:CE2 2.38	0.61
	0.59
1. A .75. A DC. HC2 1. A .70. A DC. NU1 2.15	0.58
1.A.19.ARG:HG2	0.58
1:A:73:SER:HB2 3:P:7:ARG:NH2 2.18	0.58
2:B:38:GLN:HE21 2:B:40:LEU:CD2 2.16	0.57
2:B:79:ALA:HB2 2:B:94:TYR:CD2 2.40	0.57
1:A:144:LYS:O 1:A:148:GLU:HG3 2.05	0.57
1:A:73:SER:HB2 3:P:7:ARG:CZ 2.36	0.56
2:B:15:PRO:HG3 2:B:97:ARG:HB2 1.87	0.55
2:B:81:ARG:HH12 2:B:83:LYS:CE 2.19	0.55
1:A:250:PRO:HG2 1:A:253:LYS:HB2 1.90	0.54
2:B:81:ARG:HH22 2:B:83:LYS:NZ 2.03	0.54
1:A:9:VAL:HG22 1:A:24:GLU:HG2 1.90	0.54

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A		Interatomic	Clash
Atom-1	Atom-2	$\operatorname{distance}\ (\text{\AA})$	overlap (Å)
2:B:19:LYS:HD2	2:B:20:PRO:CD	2.37	0.54
1:A:28:VAL:HG11	1:A:179:LEU:HD13	1.89	0.53
1:A:178:THR:HG21	6:A:1044:HOH:O	2.08	0.53
2:B:81:ARG:NH2	2:B:83:LYS:HZ1	2.07	0.52
3:P:7:ARG:NE	3:P:7:ARG:HA	2.25	0.52
2:B:81:ARG:NH1	2:B:83:LYS:NZ	2.55	0.51
3:P:3:ILE:HG12	3:P:4:GLU:N	2.26	0.51
1:A:174:ASN:HA	4:C:2:FUL:O3	2.11	0.51
1:A:75:ARG:NH1	1:A:79:ARG:HH12	2.09	0.50
2:B:7:ILE:HB	2:B:93:VAL:HG21	1.95	0.49
1:A:115:GLN:HG2	1:A:125:ALA:HB1	1.94	0.48
1:A:58:GLU:HB2	6:A:1057:HOH:O	2.13	0.48
2:B:38:GLN:NE2	2:B:45:LYS:HB2	2.29	0.48
6:A:1016:HOH:O	4:C:2:FUL:H63	2.14	0.48
1:A:210:PRO:O	1:A:263:HIS:HE1	1.97	0.47
1:A:154:GLU:N	1:A:154:GLU:OE1	2.48	0.47
1:A:75:ARG:NH1	1:A:79:ARG:NH1	2.64	0.46
2:B:5:PRO:HB3	2:B:30:PHE:HB3	1.98	0.46
1:A:152:GLU:OE2	1:A:155:ARG:NH2	2.47	0.45
3:P:2:GLU:HG3	3:P:3:ILE:N	2.32	0.44
1:A:191:HIS:CD2	1:A:199:VAL:HG11	2.53	0.43
2:B:48:LYS:HE3	6:B:137:HOH:O	2.19	0.43
1:A:185:PRO:HG3	1:A:208:PHE:HB3	2.01	0.43
1:A:70:ASN:O	1:A:74:PHE:HD1	2.00	0.42
2:B:21:ASN:HB3	2:B:70:PHE:CE1	2.54	0.42
1:A:191:HIS:NE2	1:A:199:VAL:HG11	2.35	0.42
1:A:196:GLU:HB2	1:A:198:LYS:NZ	2.35	0.42
1:A:110:LEU:O	1:A:111:ARG:HB3	2.18	0.42
1:A:19:GLU:H	1:A:19:GLU:CD	2.23	0.41
4:C:1:NAG:O7	4:C:1:NAG:H3	2.20	0.41
1:A:272:LEU:HD12	1:A:272:LEU:N	2.35	0.41
1:A:126:LEU:HD22	1:A:156:LEU:HD23	2.02	0.40
1:A:182:THR:HG21	1:A:265:GLY:HA2	2.03	0.40
2:B:11:SER:HA	2:B:22:ILE:O	2.21	0.40

There are no symmetry-related clashes.



5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	entiles
1	A	272/274~(99%)	263 (97%)	9 (3%)	0	100	100
2	В	97/99 (98%)	96 (99%)	1 (1%)	0	100	100
3	Р	6/8 (75%)	6 (100%)	0	0	100	100
All	All	375/381 (98%)	365 (97%)	10 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric Outliers		Percentiles		
1	A	$232/232 \ (100\%)$	226 (97%)	6 (3%)	46	50	
2	В	94/94 (100%)	93 (99%)	1 (1%)	73	79	
3	Р	7/7 (100%)	7 (100%)	0	100	100	
All	All	333/333 (100%)	326 (98%)	7 (2%)	53	59	

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	45	TYR
1	A	198	LYS
1	A	230	LEU
1	A	255	GLN
1	A	268	GLU

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Mol	Chain	Res	Type
1	A	272	LEU
2	В	56	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	72	GLN
1	A	114	GLN
1	A	115	GLN
1	A	188	HIS
1	A	220	ASN
1	A	255	GLN
1	A	263	HIS
1	A	264	GLN
2	В	38	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

2 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with |Z| > 2 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Trees	Chain	Res	Bond lengths			B	ond ang	les	
MIOI	Type	Chain	nes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	С	1	4,1	14,14,15	0.64	0	17,19,21	0.63	0
4	FUL	С	2	4	10,10,11	0.56	0	14,14,16	0.66	0



In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	С	1	4,1	-	2/6/23/26	0/1/1/1
4	FUL	С	2	4	-	-	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

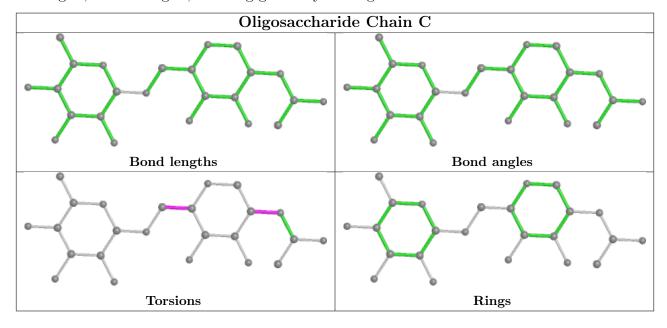
Mol	Chain	Res	Type	Atoms
4	С	1	NAG	O5-C5-C6-O6
4	С	1	NAG	C3-C2-N2-C7

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	С	1	NAG	1	0
4	С	2	FUL	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.





5.6 Ligand geometry (i)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with |Z| > 2 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

7	Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
1	VIOI					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
	5	NAG	A	801	1	14,14,15	0.70	0	17,19,21	1.05	1 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	A	801	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
5	A	801	NAG	C1-O5-C5	2.80	115.98	112.19

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	801	NAG	C1-C2-N2-C7
5	A	801	NAG	C3-C2-N2-C7

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	801	NAG	1	0



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains (i)

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

